```
<110> Hayward, Nicholas K.
      Weber, Gunther
      Grimmond, Sean
      Nordenskjold, Magnus
      Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
      SAME

<130> DAVIES

<140> 08/765,588
<141> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1
<211> 649
<212> DNA
<213> Nucleotide Sequence of VEGF165

<220>
<221> CDS
<222> (17)..(589)

<400> 1
tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt   52
                  Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
                   1               5                  10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc      100
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
            15                  20                  25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg      148
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
        30                  35                  40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac      196
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 45                  50                  55                  60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc      244
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
                 65                  70                  75
```

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg   292

Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
            80   85   90

gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg   340

Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
        95   100   105

atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag   388

Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
    110   115   120

cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa   436

His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
125   130   135   140

aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa   484

Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
            145   150   155

gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc   532

Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
            160   165   170

aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag   580

Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
            175   180   185

ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg   629

Pro Arg Arg
    190

                                                                   649
gaaccagatc tctcaccagg

<210> 2
<211> 191
<212> PRT
<213> Nucleotide Sequence of VEGF165

<400> 2
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1   5   10   15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
            20   25   30

-2-

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
        35   40   45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
    50   55   60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65   70   75   80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
            85   90   95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
            100   105   110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
            115   120   125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
    130   135   140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145   150   155   160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
                165   170   175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
            180   185   ,   190

<210> 3
<211> 1094
<212> DNA
<213> Nucleotide Sequence of SOM175

<220>
<221> CDS
<222> (3)..(623)

<400> 3
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag   47
   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
   1   5   10   15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
            20   25   30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
            35   40   45

-3-

```
cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc     191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
        50                  55                  60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt     239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
        65                  70                  75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac     287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
    80                  85                  90                  95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg     335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
                100                 105                 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa     383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
                115                 120                 125

aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac     431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
        130                 135                 140

cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca     479
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
        145                 150                 155

ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct     527
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
160                 165                 170                 175

gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc     575
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
                180                 185                 190

gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct     623
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
            195                 200                 205

tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683

agactcagca gggtgacttg cctcagaggc tatatcccag tgggggaaca aggggagcc 743
```

-4-

tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803

ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863

agagttggaa gaggagactg ggaggcagca agagggtca cataccagct caggggagaa 923

tggagtactg tctcagtttc taaccactct gtgcaagtaa gcatcttaca actggctctt 983

cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tggtacaaga 1043

actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a   1094

<210> 4
<211> 207
<212> PRT
<213> Nucleotide Sequence of SOM175

<400> 4
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1   5   10   15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
            20   25   30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
        35   40   45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
    50   55   60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65   70   75   80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85   90   95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
            100   105   110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115   120   125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
    130   135   140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
145   150   155   160

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala

-5-

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
            180   185   190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
        195   200   205

<210> 5
<211> 993
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exon 6

<220>
<221> CDS
<222> (3)..(566)

<400> 5
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag   47

    Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
     1   5   10   15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
                20   25   30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143

Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
            35   40   45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191

Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
        50   55   60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239

Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
    65   70   75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287

Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80   85   90   95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg   335

Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
                100   105   110

```
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa    383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
            115                 120                 125

aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca    431
Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
            130                 135                 140

cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc    479
Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
            145                 150                 155

cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag    527
Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
160                 165                 170                 175

ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg    576
Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
                180                 185

cttttcagac tcagcagggt gacttgcctc agaggctata tcccagtggg ggaacaaagg 636

ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag 696

gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tccctgaggc catcatcaaa 756

caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816

ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876

gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt gggctttggt 936

acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa     993


<210> 6
<211> 188
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1               5                   10                  15
```

-7-

```
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
             20                  25              30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
         35              40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
     50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
             85                  90                  95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
         100             105             110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
     115             120             125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
    130             135             140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145             150             155             160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
             165             170             175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
             180             185
```

<210> 7
<211> 858
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
<221> CDS
<222> (3)..(431)

<400> 7
```
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag      47
   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
    1             5               10              15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac      95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
             20              25                  30
```

```
cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc    143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
             35              40              45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc    191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
             50              55              60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt    239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
         65              70              75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac    287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
         80              85              90              95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg    335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
             100             105             110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa    383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
             115             120             125

aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg    431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
             130             135             140

tgacacatgg cttttcagac tcagcagggt gacttgcctc agaggctata tcccagtggg    491

ggaacaaagg ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa    551

gctgctctag gacctgggcc tctcagaggg ctcttctgcc atccttgtc tccctgaggc    611

catcatcaaa caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata    671

ccagctcagg ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat    731

cttacaactg gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt    791

gggctttggt acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa    851
```

-9-

aaaaaaa

<210> 8
<211> 143
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8

```
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1               5                   10                  15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
            20                  25                  30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
         35                  40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
     50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85                  90                  95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
            100                 105                 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115                 120                 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
    130                 135                 140
```

<210> 9
<211> 910
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
<221> CDS
<222> (3)..(305)

<400> 9

```
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag      47
   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
    1               5                   10                  15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac      95
```

-10-

```
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
                 20              25              30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
            35              40              45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
            50              55              60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
        65              70              75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
    80              85              90              95

caa gtc cgg atg cag acc taaaaaaaag gacagtgctg tgaagccaga           335
Gln Val Arg Met Gln Thr
                100

cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395

ccccggagca ccctccccag ctgacatcac ccatcccact ccagccccag gcccctctgc 455

ccacgctgca cccagcacca ccagcgccct daccccccgga cctgccgctg ccgctgccga 515

cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaacccaga cacctgcagg 575

tgccggaagc tgcgaaggtg acacatggct tttcagactc agcagggtga cttgcctcag 635

aggctatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695

cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755

ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815

gcaagagggg tcacatacca gctcagggga gaatggagta ctgtctcagt ttctaaccac 875
```

-11-

tctgtgcaag taagcatctt acaactggct cttcc

<210> 10
<211> 101
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1   5   10   15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
            20   25   30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
        35   40   45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
    50   55   60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65   70   75   80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85   90   95

Val Arg Met Gln Thr
                100

<210> 11
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 11
accaccacct ccctgggctg gcatgtggca cgtgcataaa cg   42

<210> 12
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 12
agttgtttga ccacattgcc catgagttcc atgctcagag gc   42

<210> 13
<211> 38
<212> DNA

<213> Oligonucleotide

<400> 13
gatcctgggg ctggagtggg atggatgatg tcagctgg   38

<210> 14
<211> 40
<212> DNA
<213> Oligonucleotide

<400> 14
gcgggcagag gatcctgggg ctgtctggcc tcacagcact   40

<210> 15
<211> 236
<212> DNA
<213> Human SOM175

<400> 15
atgaggggcc aggtacgtga ggtctcccac aggcccctgg aaagaatact tacatctgct 60

cccatggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagtcttt ctcctccgta ggctgcctcc agccccaggc 180

cccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga   236

<210> 16
<211> 1242
<212> DNA
<213> mVRF

<220>
<221> CDS
<222> (166)..(789)

<400> 16
gcacgagctc aggccgtcgc tgcggcgctg cgttgcgctg cctgcgccca gggctcggga 60

ggggccgcg gaggagccgc ccctgcgcc ccgccccggg tccccgggtc cgcgccatgg 120

ggcggctctg gctgacccccc ccccacaccg ccgggctagg gcccg atg agc ccc ctg 177
                                              Met Ser Pro Leu
                                                1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

-13-

Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu Ala Arg Thr Gln
 5   10   15   20

gcc cct gtg tcc cag ttt gat ggc ccc agt cac cag aag aaa gtg gtg   273

Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln Lys Lys Val Val
               25   30   35

cca tgg ata gac gtt tat gca cgt gcc aca tgc cag ccc agg gag gtg   321

Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln Pro Arg Glu Val
               40   45   50

gtg gtg cct ctg agc atg gaa ctc atg ggc aat gtg gtc aaa caa cta   369

Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val Val Lys Gln Leu
               55   60   65

gtg ccc agc tgt gtg act gtg cag cgc tgt ggt ggc tgc tgc cct gac   417

Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys Cys Pro Asp
         70   75   80

gat ggc ctg gaa tgt gtg ccc act ggg caa cac caa gtc cga atg cag   465

Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val Arg Met Gln
 85   90   95   100

atc ctc atg atc cag tac ccg agc agt cag ctg ggg gag atg tcc ctg   513

Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly Glu Met Ser Leu
               105   110   115

gga gaa cac agc caa tgt gaa tgc aga cct aaa aaa aag gag agt gct   561

Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys Glu Ser Ala
               120   125   130

gtg agg cca gac agg gtt gcc ata ccc cac cac cgt ccc cag ccc cgc   609

Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg
               135   140   145

tct gtt ccg ggc tgg gac tct acc ccg gga gca ccc tcc cca gct gac   657

Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp
               150   155   160

atc atc cat ccc act cca gcc cca gga tcc tct gcc cgc ctt gca ccc   705

Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro
165   170   175   180

agc gcc gcc aac gcc ctg acc ccc gga cct gcc gtt gcc gct gta gac   753

Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp

-14-

```
gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc    799
Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
            200                 205

agacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacgggc 859

ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacctcct 919

cagtctggga ggtcactgcc ccaggacctg dacctttttag agagctctct cgccatcttt 979

tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctcaggggcc 1039

agggtactct ctcacttaac caccctggtc aagtgagcat cttctggctg gctgtctccc 1099

ctcactatga aaaccccaaa cttctaccaa taacgggatt tgggttctgt tatgataact 1159

gtgacacaca cacacactca cactctgata aaagagatgg agacactaaa aaaaaaaaaa 1219

                                                              1242

aaaaaaaaaa aaaaaaaaaa aaa
```

<210> 17
<211> 207
<212> PRT
<213> mVRF

```
<400> 17
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
1               5               10              15
Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
            20              25              30
Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
        35              40              45
Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
    50              55              60
Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65              70              75              80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
            85              90              95
Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
        100             105             110
Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115             120             125
Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
    130             135             140
```

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro
145   150   155   160
Ser Pro Ala Asp Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala
            165   170   175
Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val
            180   185   190
Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
            195   200   205

<210> 18
<211> 188
<212> PRT
<213> mVRF167

<400> 18
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
1   5   10   15

Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
            20   25   30

Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
            35   40   45

Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
        50   55   60

Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65   70   75   80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85   90   95

Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
            100   105   110

Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
            115   120   125

Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro
            130   135   140

Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145   150   155   160

Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu
                165   170   175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys
                180   185

<210> 19
<211> 188

<212> PRT
<213> hVRF167

<400> 19

```
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1               5                   10                  15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
            20                  25                  30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
        35                  40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
    50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85                  90                  95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
            100                 105                 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115                 120                 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
    130                 135                 140,

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145                 150                 155                 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
                165                 170                 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
                180                 185
```

<210> 20
<211> 71
<212> PRT
<213> mVRF186

<400> 20

```
Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
 1               5                   10                  15

Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro
            20                  25                  30

Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn
        35                  40                  45
```

-17-

```
Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser
    50                  55                  60

Ser Ile Ala Lys Gly Gly Ala
65                  70


<210> 21
<211> 71
<212> PRT
<213> hVRF186

<400> 21
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
  1             5                  10                  15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
            20                  25                  30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
        35                  40                  45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Asp Ala Ala Ala Ser
    50                  55                  60

Ser Val Ala Lys Gly Gly Ala
65                  70


<210> 22
<211> 214
<212> PRT
<213> mVEGF188

<400> 22
Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
  1             5                  10                  15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
            20                  25                  30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
        35                  40                  45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
    50                  55                  60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
65                  70                  75                  80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
            85                  90                  95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
            100                 105                 110
```

```
Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
        115                 120             125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg
    130             135             140

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys
145             150             155             160

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu
            165             170             175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp
            180             185             190

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
        195             200             205

Cys Asp Lys Pro Arg Arg
    210
```